Amendments to the Claims:

1. (Currently amended) An antibacterial compound consisting of a substantially uncharged morpholino antisense oligomer containing from ~~8~~ 10 to 40 nucleotide subunits, each of said subunits comprising a morpholino ring supporting a base-pairing moiety effective to bind by Watson-Crick base pairing to a respective nucleotide base, said base-pairing moieties including a targeting nucleic acid sequence at least 10 nucleotides in length which is able to stably hybridize ~~complementary~~ to a bacterial 16S or 23S rRNA nucleic acid sequence, wherein

~~each of said subunits comprises a 5- or 6-membered ring supporting a base-pairing moiety effective to bind by Watson-Crick base pairing to a respective nucleotide base in the bacterial nucleic acid sequence, and~~

adjacent subunits are linked together by phosphorous-containing linkages, one to three atoms long, joining the morpholino nitrogen of one subunit to the 5' exocyclic carbon of an adjacent subunit, and ~~joined by uncharged linkages selected from the group consisting of: uncharged phosphoramidate and phosphorodiamidate, carbonate, carbamate, amide, phosphotriester, alkyl phosphonate, siloxane, sulfone, sulfonamide, sulfamate, thioformacetyl, and methylene-N-methylhydroxylamino, or by charged linkages selected from the group consisting of phosphate, charged phosphoramidate and phosphorothioate, wherein~~ the ratio of uncharged linkages to charged linkages in the oligomer is at least [[4]]5:1.

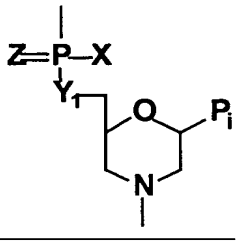
2. (Original) The compound of claim 1, wherein said oligomer is able to hybridize with the bacterial sequence at a Tm substantially greater than the Tm of a duplex composed of a corresponding DNA and the same bacterial sequence.

3. (Original) The compound of claim 1, wherein said oligomer is able to hybridize with the bacterial sequence at a T_m substantially greater than 37°C.

4. (Currently amended) The compound of claim 1, wherein said bacterial nucleic acid sequence is a 16S or 23S rRNA nucleic acid sequence of one of more bacteria selected from the group consisting of *Escherichia coli, Salmonella thyphimurium, Pseudomonas*

aeruginosa, Vibrio cholera, Neisseria gonorrhoea, Staphylococcus aureus, Mycobacterium tuberculosis, Helicobacter pylori, Streptococcus pneumoniae, Treponema palladium, Chlamydia trachomatis, Bartonella henselae, Hemophilis influenza, Shigella dysenterae, Enterococcus faecium, and *Listeria monocytogenes* ~~oligomer is a morpholino oligomer~~.

5. (Currently amended) The compound of claim 1, wherein each ~~the~~ uncharged linkage~~s are selected from the group consisting of the structures presented in Figures 2A through 2D~~ is an uncharged phosphorodiamidate linkage, in accordance with the structure below, where X=NR_2, R is hydrogen or methyl, Y_1 = O, Z = O, and P_i is a purine or pyrimidine base pairing moiety effective to bind, by base specific hydrogen bonding, to a base in a polynucleotide.



6. (Currently amended) The compound of claim 5, wherein each ~~un~~charged linkage, if present, is a linkage in accordance with the structure of claim 4, wherein X is oxide ($-O^-$) or sulfide ($-S^-$) ~~phosphorodiamidate linkage as represented at Figure 2B, where X=NR_2, where R is hydrogen or methyl, Y=O, and Z=O~~.

7. (Currently amended) The compound of claim [[4]] 5, wherein each linkage is a phosphorodiamidate linkage as represented therein ~~at Figure 2B, where X=NR_2, where R is hydrogen or methyl, Y=O, and Z=O~~.

8. (Currently amended) The compound of claim 1, wherein the region of complementarity with the target RNA sequence has a length of 13 to 20 bases ~~the ratio of uncharged linkages to charged linkages in the oligomer is at least 8:1~~.

9. (Original) The compound of claim 1, wherein the antisense oligomer has a length of from 12 to 25 subunits.

10. (Currently amended) The compound of claim ~~7~~ 9, having a length of 15 to 20 subunits.

11. (Original) The compound of claim 1, wherein the targeting sequence is selected from the group consisting of SEQ ID NOs: 15, 16, and 21-25.

12. (Original) The compound of claim 1, where the targeting sequence is complementary to a Gram-positive bacterial 16S rRNA consensus sequence or a Gram-negative bacterial 16S rRNA consensus sequence.

13. (Original) The compound of claim 12, where the targeting sequence is selected from the group consisting of SEQ ID NOs: 27-30.

14. (Original) The compound of claim 1, wherein the targeting sequence is SEQ ID NO: 92.

15. (Currently amended) A method of treating a bacterial infection in a human or mammalian animal subject, comprising

administering to the subject, in a pharmaceutically effective amount, a substantially uncharged morpholino antisense oligomer containing from ~~8~~ 10 to 40 nucleotide subunits, each of said subunits comprising a morpholino ring supporting a base-pairing moiety effective to bind by Watson-Crick base pairing to a respective nucleotide base, said base-pairing moieties including a targeting nucleic acid sequence at least 10 nucleotides in length which is able to stably hybridize ~~complementary~~ to a bacterial 16S or 23S rRNA nucleic acid sequence, wherein

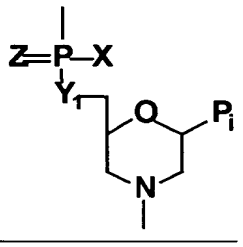
~~each of said subunits comprises a 5- or 6-membered ring supporting a base-pairing moiety effective to bind by Watson-Crick base pairing to a respective nucleotide base in the bacterial nucleic acid sequence, and~~

adjacent subunits are linked together by phosphorous-containing linkages, one to three atoms long, joining the morpholino nitrogen of one subunit to the 5' exocyclic carbon of an adjacent subunit, and ~~joined by uncharged linkages selected from the group consisting of: uncharged phosphoramidate and phosphorodiamidate, carbonate, carbamate, amide, phosphotriester, alkyl phosphonate, siloxane, sulfone, sulfonamide, sulfamate, thioformacetyl, and methylene-N-methylhydroxylamino, or by charged linkages selected from the group consisting of phosphate, charged phosphoramidate and phosphorothioate, wherein~~ the ratio of uncharged linkages to charged linkages in the oligomer is at least [[4]]5:1.

16. (Original) The method of claim 15, wherein said oligomer is able to hybridize with the bacterial sequence at a T_m substantially greater than 37°C.

17. (Currently amended) The method of claim 15, wherein the bacterial nucleic acid sequence is a 16S or 23S rRNA nucleic acid sequence of one of more bacteria selected from the group consisting of *Escherichia coli*, *Salmonella thyphimurium*, *Pseudomonas aeruginosa*, *Vibrio cholera*, *Neisseria gonorrhoea*, *Staphylococcus aureus*, *Mycobacterium tuberculosis*, *Helicobacter pylori*, *Streptococcus pneumoniae*, *Treponema palladium*, *Chlamydia trachomatis*, *Bartonella henselae*, *Hemophilis influenza*, *Shigella dysenterae*, *Enterococcus faecium*, and *Listeria monocytogenes* ~~oligomer is a morpholino oligomer~~.

18. (Currently amended) The method of claim 16, wherein each ~~the~~ uncharged linkage~~s are selected from the group consisting of the structures presented in Figures 2A through 2D~~ is an uncharged phosphorodiamidate linkage, in accordance with the structure below, where X=NR_2, R is hydrogen or methyl, Y_1 = O, Z = O, and P_i is a purine or pyrimidine base pairing moiety effective to bind, by base specific hydrogen bonding, to a base in a polynucleotide.



19. (Currently amended) The method of claim 18, wherein each ~~un~~charged linkage, if present, is a linkage in accordance with the structure of claim 4, wherein X is oxide ($-O^-$) or sulfide ($-S^-$) ~~phosphorodiamidate linkage as represented at Figure 2B, where X=NR_2, where R is hydrogen or methyl, Y=O, and Z=O~~.

20. (Currently amended) The method of claim ~~17~~ 18, wherein each linkage is a phosphorodiamidate linkage as represented therein ~~at Figure 2B, where X=NR_2, where R is hydrogen or methyl, Y=O, and Z=O~~.

21. (Original) The method of claim 15, where the antisense oligomer has a length of from 12 to 25 bases.

22. (Currently amended) The method of claim 17, wherein the the region of complementarity with the target RNA sequence has a length of 13 to 20 bases ~~oligomer has a length of from 15 to 20 bases~~.

23. (Original) The method of claim 15, wherein the targeting sequence is selected from the group consisting of SEQ ID NOs: 15, 16 and 21-25.

24. (Original) The method of claim 15, where the targeting sequence is complementary to a Gram-positive bacterial 16S rRNA consensus sequence or a Gram-negative bacterial 16S rRNA consensus sequence.

25. (Original) The method of claim 24, where the targeting sequence is selected from the group consisting of SEQ ID NOs: 27-30.

26. (Original) The method of claim 21, for use in treatment of an infection produced by *E. coli, Salmonella thyphimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria gonorrhoea, Helicobacter pylori, Bartonella henselae, Hemophilis Influenza, Shigella dysenterae, Staphylococcus aureus, Mycobacterium tuberculosis, Streptococcus pneumoniae, Treponema palladium and Chlamydia trachomatis,* where the antisense oligomer has a sequence selected from the group consisting of SEQ ID NOs: 21-25.

27. (Original) The method of claim 15, wherein the antisense oligomer is administered in an amount and manner effective to result in a peak blood concentration of at least 200-400 nM antisense oligomer.

28. (Original) The method of claim 15, for treating bacterial infections of the skin, wherein said administering is by a topical route.

29. (Original) The method of claim 12, for use in treating a bacterial respiratory infection, wherein said administering is by inhalation.

30. (Currently amended) A livestock and poultry food composition containing a food grain supplemented with a subtherapeutic amount of an antibacterial compound, said compound consisting of a substantially uncharged morpholino antisense oligomer containing from ~~8~~ 10 to 40 nucleotide subunits, each of said subunits comprising a morpholino ring supporting a base-pairing moiety effective to bind by Watson-Crick base pairing to a respective nucleotide base, said base-pairing moieties including a targeting nucleic acid sequence at least 10 nucleotides in length which is able to stably hybridize ~~complementary~~ to a bacterial 16S or 23S rRNA nucleic acid sequence, wherein

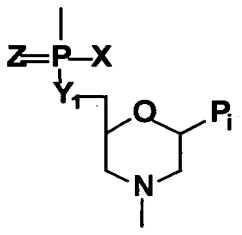
~~each of said subunits comprises a 5- or 6-membered ring supporting a base-pairing moiety effective to bind by Watson-Crick base pairing to a respective nucleotide base in the bacterial nucleic acid sequence, and~~

adjacent subunits are linked together by phosphorous-containing linkages, one to three atoms long, joining the morpholino nitrogen of one subunit to the 5' exocyclic carbon of an adjacent subunit, and ~~joined by uncharged linkages selected from the group consisting of: uncharged phosphoramidate and phosphorodiamidate, carbonate, carbamate,~~

~~amide, phosphotriester, alkyl phosphonate, siloxane, sulfone, sulfonamide, sulfamate, thioformacetyl, and methylene-N-methylhydroxylamino, or by charged linkages selected from the group consisting of phosphate, charged phosphoramidate and phosphorothioate, wherein~~ the ratio of uncharged linkages to charged linkages in the oligomer is at least [[4]]5:1.

31. (Currently amended) The composition of claim 30, wherein the bacterial nucleic acid sequence is a 16S or 23S rRNA nucleic acid sequence of one of more bacteria selected from the group consisting of *Escherichia coli*, *Salmonella thyphimurium*, *Pseudomonas aeruginosa*, *Vibrio cholera*, *Neisseria gonorrhoea*, *Staphylococcus aureus*, *Mycobacterium tuberculosis*, *Helicobacter pylori*, *Streptococcus pneumoniae*, *Treponema palladium*, *Chlamydia trachomatis*, *Bartonella henselae*, *Hemophilis influenza*, *Shigella dysenterae*, *Enterococcus faecium*, and *Listeria monocytogenes* ~~oligomer is a morpholino oligomer~~.

32. (Currently amended) The composition of claim 31, wherein each linkage is a phosphorodiamidate linkage ~~as represented at Figure 2B~~, in accordance with the structure below, where X=NR_2, where R is hydrogen or methyl, Y=O, and Z=O, and P_i is a purine or pyrimidine base pairing moiety effective to bind, by base specific hydrogen bonding, to a base in a polynucleotide.



33. (Original) The composition of claim 30, wherein the antisense oligomer has a length of from 12 to 25 bases.

34. (Original) The composition of claim 30, wherein the targeting sequence is selected from the group consisting of SEQ ID NOs: 15, 16, 21-25 and 27-30.